Changed the margins in cases where the sequence text was "wrapped" down to the next line. Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted to applicant was the prior application data; or other Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" (field. The applicant spelled out a number instead of using an inchanged the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at e page numbers throughout text; other invalid text, such as Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.		Changed a file from non-ASCII to ASCII ENTERED.
Edited the Current Application Data section with the actual current number. The number inputted to applicant was the prior application data; or other Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" (field. The applicant spelled out a number instead of using an inchanged the spelling of a mandatory field (the headings or subheadings), specifically; Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at empage numbers throughout text; other invalid text, such as inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.		Changed the margins in cases where the sequence text was "wrapped" down to the next line.
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Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the policiant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted:		Edited the "Number of Sequences" (ield. The applicant spelled out a number instead of using an integer
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Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.		Corrected an obvious error in the response, specifically:
A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.		Edited identifiers where upper case is used but lower case is required, or vice versa.
		Corrected an error in the Number of Sequences field, specifically:
and adjusted the "(A)) engin; field accordingly	_	A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
Deleted ending stop cocon in amino acid sequences and adjusted the (A)congili. Held december 3. due to a Patentin bug). Sequences corrected:	C	Deleted ending stop codon in amino acid sequences and adjusted the *(A)Length:* field accordingly (err
Other: Authorized edit: Soquence # 14, changed lengt.	-	Other: Authorized edit: Sequence # 14, changed length

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

1652

RAW SEQUENCE LISTING DATE: 10/11/2000 PATENT APPLICATION: US/09/202,681A FIME: 16:29:36

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```
SEQUENCE LISTING
      1 (1) GENERAL INFORMATION:
              (i) APPLICANT: Recombinant Biocatalysis: Inc.
           (ii) TITLE OF INVENTION THERMOSTABLE PHOSPHATASES (iii) NUMBER OF SEQUENCES: 54
            (17) CORPESPONDENCE ADDRESS:
                  (A) APPERSEFE: Fish & Pichardson P.C.
                   (B) STREET, 4225 Executive Square, Suite 1400
     1.1
                   (€) CIN: La Joilt
                   (b) STAIE: CA
                   (E) COUNTRY: USA
            (F) DIP: 92037
(H) COMPUTER PEADABLE FORM:
     į g
                   (A) MEDIUM TYPE: Diskette
                   (B) COMPUTER: IBM Compatible
                   (C) OPERATING SYSTEM: Windows 95
                   (D) SCHIWAPE: PastSEQ for Windows Version 2.0b
           ("1) CURRENT APPLICATION DATA:
                   (A) APPLICATION NUMBER: US/09/202,681A
                   (B) FILING DATE: 23-Dec-1999
C--> 28
                   (C) CLASSIFICATION:
     29
           (CEL) PRIOR APPLICATION DATA:
     5 i
                   (A) APPLICATION NUMBER: 08 '666.85%
                   (B) FILING DATE: 19-JUN-1036
                   (A) APPLICATION NUMBER: 50/033.752
                   (B) FILING DATE: 19-JUN-1997
          (wili) ATTURNEY/AGENT INFORMATION:
                   (A) NAME: Haile, Ph.D. Lisa A
      4 ..
                   (b) REGISTRATION NUMBER: 38.347
     10
                   (C) REFERENCE/DCCKET NUMBER: 09010/015W01
     11
           (1%) TELEC.MMUNICATION INFORMATION:
     13
                   (A) TELEPHONE: 619/678-3070
     14
                   (B) TELEFAX: 619/678-5099
     15
                    (P) TELEX:
     16
     18 (U) INFORMATION FOR SEQ ID NO:
             (1) SEQUENCE CHARACTELISTICS:
     50
                   (A) (ENGTH: 52 base pairs
     5 L
                   (B) TYPE: nucleic acid
                   (C) STPANDEDNESS single
     53
           (E) FORENDOSY: Litear
(ii) MOLLOULE TYPE: oDBA
(xi) DEQUENCE DESCRIPTION: SEQ ID NO: 1:
     5 L
     36
     : 14
     80 COGAGANTO ATTANAGAGG AGATATTAAC TATGGGGGGA GGTCCGAAAA GG
     83 (L) INFORMATION FOR SEC ID NO: 2:
             (i) SEQUENCE CHARACTERISTICS:
     5.1
                   (A) LENGTH. 31 bace pairs
     4.15
     5.0
                   (B) TYPE: nucleic acid
```

RAW SEQUENCE LISTING DATE: 10/11/2000 FATENT APPLICATION: US/09/202,681A ITME: 10/11/2000

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(C) SIPANDEDNESS: single
                      (D) TOPOLOGY: limear (II) MOLECULE TYPE: CONF
\mathbb{T}\mathfrak{J}
(1) MODESTHE THE COME

(X1) SECTION ELECTRIPTION (SECTION)

(X2) SECTION ELECTRIPTION (SECTION)

(X3) COMPANY ELECTRIPM (SECTION)

(X4) COMPANY ELECTRIPM (SECTION)

(X5) COMPANY ELECTRIPM (SECTION)

(X6) COMPAN
                                                                                                                                                                                                                                                   11
                                       (A) LENGIH: 32 mase pairs
 ٠,
 80
                                           (B) PYPE: nucleic acid
                                         (C) STRANDEL-KESS: single
                 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDN.
86 (XI) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
88 CCGAGAATTC ATTAAAGAGG AGAAATTAAA TATGTTGGAT ATACTGCITG IT
90 (2) INFORMATION FOR SLQ ID WO: 4: 32 (1) SEQUENCE CHARACTERISTICS:
93
                                         (A) LENGTH: 32 base pairs
                                           (b) TYPE: nucleic acid
                                           (C) STPANDEDNESS: single
                (ii) MOLECULE TYPE: cDN4
 G.G
 98
                         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
102 COSMITATION THAILITTELA ACCIDATED CC
104 (2) INFORMATION FOR NEQ 10 NO: 5:
106 (1) SEQUENCE CHARACTERISTICS:
 107
                                           (A) LENGTH: of base pairs
                                              (B) PYPE: nacleic acid
 108
                                              (C) STRANDEDNESS: single
                                             (D) TOPOLOGY: linear
 110
                     (ii) MOLECULE TYPE: CUNA
                           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 116 CCCACAATIG ATTAAACAGG AGRAATTAAC TATGATGATG GAATTCACTC GC
 119 (2) INFORMATION FOR SEQ II NO: 6:
120 (1) SEQUENCE CHARACTERISTICS:
121 (A) LENGTH: 3) Fase pairs
                                               (B) TYPE: nucleic acid
                       (C) STRANDEDNES: single
(D) TOPOLOGY: l:near
(ii) MOLECULE TYDE: cDNA
 (31) SEGMENTE DESCRIPTION: SEQ ID NO: 6: 126 COMMIGNATION CHARACTERS ANALYSIST IA
 1:2 (2) INFORMATION FOR SEQ ID NO: 7:
1;4 (1) SEQUENCE CHARACTERISTICS:
 135
                                         - (A) LENGTH: 52 base pairs
                                             FB) TYPE: musleuc acid
                                            (C) STRANDERNESS: single
                   (b) TOPOLOGY: linear
(xi) MOLECULE TYPE: DDMA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 158
 140
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PAW SEQUENCE LISTING DATE: 10/11/2000 EATENT APPLICATION: US/09/202,681A TIME: 16:29:36

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```
144 COGACAATTG ATTAAAGAGG AGARATTAAC TATGAGARACC CIGACAATAA AC
                                                                                       5.2
115 (2) INFORMATION FOR SEQ 10 NO: 8:
          (1) SEQUENCE CHARACTETISTICS:
118
                (A LENGTH: 31 base pairs
119
                (B: TYPE: nuclei: acid
150
                (C STRANDEDNESS single (D. TOPOLOGY: linear
151
151
        (11) MOLECULE TYPE: CONA
         (xi) SEQUENCE DESCRIPTION: SEQ 1D No. 3:
Loo
TUB COGADDATCO ITACACCOAC AGANCOCTTA C
                                                                                        3.1
160 (2) INFORMATION FOR SEQ ID NO: 9:
        (1) SEQUENCE CHARACTERISTICS
102
               'A) LENGTH: 52 base pairs
ins
                 B) TYPE: nucleic acid
144
                 C) STRANDEDNESS: single
165
                 (D) TOPOLOCY: linear
      (ii) MOLECULE TYPE: CLNA
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                       5.3
1"2 COGAGAATTO ATTAAAGAGG ACAATTAAC TATGAAAGGA AAGTOTOTTG TT
104 (1) INFORMATION FOR SEQ II NO: 10: 16: 6 (1) SEQUENCE CHARACTEPISTICS:
               (A) LENGIH 31 base pairs
               (E) TYPE: nucleur acid
               () SIRANDEDNESH: single
        (i) TOPOLOGY: ..near
(ii) MOLECULE TYPE: OFNA
180
         (XI) SERVENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                        3.1
186 CUGAGGATCO TOAAGCTTIC TGGAGAAICA A
188 (2) INFORMATION FOR SEQ TO NO: 11:
        (1) SEQUENCE CHARACTERISTICS:
                ( ) IENGTH: 52 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
19.1
                (D) TOPCLOGY: Linear
       (ii) MOLECULE TYPE: CONA
 66
[93 (NI) SEQUENCE DESCRIPTION: SEQ 10 NO: 11:
208 COGREGACIO ATTARAGAGE AGRAPATIANU INTEGCARGA ARTATOGOCO CT 52
202 (3) INFORMATION FOR SEQ ID NO: 12.
204 (1) SEQUENCE CHARACTERISTICS:
          (A) LENGTE: 34 base pairs
205
                (B) TYFE: nucleic arid
               (C) STRANDEDNESS: single
208 (D) TOPOLOGY linear
210 (ii) MOLECULE TYPE CDNA
212 (Xi) SEQUENCE DESCRIPTION: SEQ 1D NO: 12:
214 CCGAOGATIC TRANSCETTE TOGAGGTOGG GGTT
215 (D) INFERENCE DESCRIPTION: SEQ 1D NO: 12:
216 (2) IMFORMATION FOR SEQ ID NO: 13:
       (i) SEQUENCE CHARACTERISTICS:
218
219
               (A) LENGTH: 54 base pairs
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RAW SEQUENCE LISTING DATE: 10/11/2000 PATENT APPLICATION: US/09/202,681A TIME: 10:20:36

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```
(B) PYPE: nucleic acid
220
               (C) STRANDEDNESS single
221
222
                (D) TOPOLOGY: linear
224
        (11) MOLLOULE TYPE: COLA
         (E1) SEQUENCE PESCHIPITON: . EQ ID NO: 13:
226
208 COGACARIO STEAAAGAGI AGAZATTALO FATGTATAAA TGGAFTAIFG AGGG
230 (2) INFORMATION FOR SETTION NO. .4:
       (i) SEQUENCE CHAPACTFLISTI'S:
232
               (A) LENGTH: 31 base pairs
233
5.34
               (B) TYPE: nurleis acit
                (C) STRANDEDNESS single
235
      (D) TOPOLOGY li mear
(ii) M-LECCLE TYPE CLUA
336
238
         (x) SEQUENCE DESCRIPTION: SEQ 10 NO: 11.
240
242 CCGACGACTA AACATAGICE AAGTAATTKG C
                                                                                       0.1
244 (.) INFORMATION FOR SET ID NO: .:
        (i) SEQUENCE CHARACTERISTICS:
246
                (A) LINGTH: 52 base pairs
217
2.18
                (B) TYPE: nuclei: acii
        (C) STRANDEDNESS, single
(D) TOPOLOGY: linear
(ii) MELECOLE TYPE: cDMA
249
250
330
254 (XI) SECUENCE DESCRIPTION: SEQ ID NO: 15:
256 CCGAJAAITC ATTAAAGAGA AGAMATTAAC TAMGAGAATC CICCTCACCA AC 50
258 (2) INFORMATION FOR SEQ ID NO: 16:
        (1) SEQUENCE CHARACTERISTICS:
260
               (A) LFNGTH: 31 Lise pairs (B) TYPE: musleic acid
26.
260
                (C) STEANDETNESS: single
260
      (D) TOPOLOGY: Tinear
(II) HOLECULE TYPE: cDNA
264
26€
266 (xi) SEVERGE PROFIFTION, SEQ ID NO: 16: 500 COGAGGATCC PRACAGGIC AGAAGCCTTF G
274 (1) SEQUENCE CHARACTERISTICS:
27 5
               (A) LENGIE: 31 base pairs
                (B) TYPE: nucleic acid
370
                (C) STRANDELNESS: single
       (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Genomic DNA
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
280
23.2
281 CCGAGRATIC ATTRAAGACG AGRAATTRAC TATGGAAAAC TIRAAAAAACT ACCT
286 (2) INFORMATION FOR SEQ ID NO: 18: (i) SEQUENCE CHAPACTERISTICS:
                (A) LENGIH: 31 base pairs
239
290
                (B) TYPE: mucleic acid
                (C) STRANDELNESS: single
291
                (P) TCPOLOGY: linear
292
     (ii) MGLECULE TYPE: CDMA
294
```

RAW SEQUENCE LISTING DATE: 10/11/2008 PATENT APPLICATION: US/09/202,681A TIME: 10:20:30

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298				(2.12.5.1)		n NES	coro	er tekn	. 95	a tr	NO:	18.						
(1) SEQUENCE CHARACIESISTICS: (2) SEQUENCE CHARACIESISTICS: (3) (2) SEQUENCE CHARACIESISTICS: (4) (5) TAPEL DUC eig and (5) (6) TAPEL DUC eig and (6) (7) TAPEL DUC eig and (7) MALECULE TYPE: Genomic BUA (8) SEQUENCE DESCRIPTION: SUGING (12) SEQUENCE DESCRIPTION: SUGING (13) SEQUENCE DESCRIPTION: SUGING BOX (14) (2) NAME/NEY: Coding Sequence (15) SEQUENCE DESCRIPTION: SUGING BOX BAY GAT	246	(X1)	naa a	I E N C E	יוריבירי. יוריביריי	יים ביים דים ביים	пасас	amaa	: C								3.1
(1) SEPTEMPE CHERACTERISTICS: (3) (A) LANGHT AS BASE pairs (4) (B) TYPE: DUC etc duid (5) (C) STRAMPENNISS: Single (6) (D) TOPODOWY: linear (7) (MALEXULE TYPE: Genomic PRA (8) (II) MALEXULE TYPE: Genomic Pra (8	298	Theographical for SPG ID NO: 19:																
(A) LENNTH (3 base pairs (C) STRANDFLNESS: single (C) STRANDFLNESS: single (D) TOPOJOST: Time: (D) TOPOJOST: (D) TOPOJOST: Time: (D) TOPOJOST: (D) TOPOJ		AND SECURIOR CHARACTERISTICS:																
(E) TYPE: nuclear acid (C) STRANPLANES: single (D) TOPOLOGY: Tinear (A) (II) MOLECULE TYPE: Genomic BNA (II) FETURE: (II) FETURE: (II) (A) MAME/KEY: Coding Sequence (II) (S) SECRENCE DESCRIPTION: SEG 10 No: 19: (II) ATO AGG GOG AGG GCA GTG GGG ATA STT C.CC AGG AAC GTT GAG GGG AIC III (SI) SECRENCE DESCRIPTION: SEG 10 No: 19: (II) MCL AGG GOG AGG GCA GTG GGG ATA STT C.CC AGG AAC GTT GAG GGG AIC III GCG GAG GGT GTG GGG GCT CTG CGC AAC GTT GAG GGC AIC III GCG GAG GGT GTG GGG GCT CTG CGC AAC GTT GAG GAG GCT GTG III GCG GAG GGT GTG GGG GCT CTG CGC AAC AC GTT GAG GGC AIC III GCG GAG GGT GTG GGG GCT CGC GAG CGT AGG GCC GAG CCT GCC III GCG GAG GGT GTG GCT CCC GGC GGG GGT ACC GCC GAG CAC III GCG GAG GGT CCC GGC GGC GGG GGT ACC GCC AGC CAC III GCG GAG GGT CAC GGT GCC CGG GGG GGG GGT ACC GCC AGC CAC III GCG ACC CTT TAC GTG GGG GCC CCG GGG GGG GGG GGG AGC GAT ACC III GCG ACC GTT CAC GGT GCC CGG GGG GGG GGG GGG GGC AGC GAT III GCG GGG ACC GGT CAC GGT GGG GGG GGG GGG GGG GGG GGG GGG GG		(A) LENGTH (83 base pairs																
(C) STRAMPLENISS: Single (D) TO-POLOGY: Timed (II) MALECULE TYPE: Genomic PNA (II) MALECULE TYPE: Genomic PNA (II) (EX) REFIGEE: (R) LOCATION: 1. 780 (II) (S) SECURICE DESCRIPTION: SEC ID NO: 19: (II) (S) SECURICE DESCRIPTION: SEC ID NO: 19: (III) (S) SECURICE DESCRIPTION: 19: (III) (S) SECUR																		
(ii) MOLECULE TYPE: Genomic DNA (ii) MOLECULE TYPE: Genomic DNA (ii) SECTION: (ii) SECTION: (iii) SECTION:										e								
(ii) MolECULE TYPE: Genomic DNA (iii) MEFITURE: (iii) MEFITURE: (iii) MEFITURE: (iii) MERICKEY: Coding Sequence (iii) MERICKEY: Coding Sequence (iii) SEQUENCE DESCRIPTION: SLO ID NO: 19: (iv) SEQUENCE DESCRIPTION: SLO ID NO: 19: (iv) SEQUENCE DESCRIPTION: SLO ID NO: 19: (iv) AND AGG GGG AGG GGG GGG ATA CTT COC AGC AAC GAT GAC GGC AIC (iv) SEQUENCE DESCRIPTION: SLO ID NO: 19: (iv) ATG AGG GGG AGG GGG GGG GGG ATA CTT COC ACC AAC GAT GAC GGC AIC (iv) MET AGG GGG AGG GGG GGG GGG CGG ATA CTT COC ACC AAC GAT GAC GGC AIC (iv) Met AGG GGT GGG GGT CGG GGG CAAA ACG CGG AGA GCC GIG GGT (iv) Phe Ala Gla Gly Lee Gly Ala Lee Ara 12: Met Lee Gu Pro Val Ala (iv) Phe Ala Gla Gly Lee Gly Ala Lee Ara 12: Met Lee Gu Pro Val Ala (iv) Phe Ala Gla Gly Lee Gly CCC GG CGG GGG GGG GAG GAG CAT (iv) Phe Ala Gla GGG GGG GGC GGG GGG GGG GAG GAG GAT (iv) Phe Ala Gla Tyr Val Val Ali Pro Asp Aig Glu Ara Sor ala Aia Ser His (iv) No. 15 (iv) AGC CCC AGG GTT CAC CG2 CGC CGG GGG GGG GAG GGG GAG GGG GAT (iv) AGC CCC AGG GTT CAC CG2 CGC CGG GGG GGG GAG GGG GAT ITT CGC (iv) AGC CCC AGG GTT AAA GGT TGG GTA GTG GGG GAA GGG GAG GGG GAG GGG (iv) AGC CCC AGG CTT AAA GGT TGG GTA GTG GAA GGT CCC GGC GGA GAT GGC (iv) AGC CCC AGG CTT AAA GGT TGG GTA GTG GAA GGT CCC GGC GAA GAT GAC (iv) AGC CCC AGG CTT AAA GGT TGG GTA GTT TTG CCC GAA GAT TTC CTG (iv) AGC CCC AGG CTT GAG GAG GTA CTT TTG CCC GAA GTT CCC (iv) AGC CCC AGG GTT GAG GGA GAA CTT TTG CCC GAA GTT CCC (iv) AGC CCC AGG GTT GAG GGA GGA GTA CTT TTG CCC GAA CTT CCC (iv) AGC CCC AGG GTT GGG GGG GCC AAC CTC GTG AGT ACC CGC GAC GTT TAC (iv) AGC CCC AGG GGT GGG GCG GAA CTC GGG GAA CTC GGG GAA CTC GGG (iv) AGC CCC AGG GGG GGG GGG GGG GGA GGG GGG																		
(ix) MAME/REY: Coding Sequence (ii) (A) MAME/REY: Coding Sequence (iii) (A) ECCURITOR DESCRIPTION: SEC ID No: 19: (iv) SEQUENCE DESCRIPTION: SEC ID No: 19: (iv) ATG AGG GOG AGC GAA GTG CGG ATA GTG CAC AAC GTG GAC GGC ATC (ii) Met Arg GTy Ser GTy Va. Arg The Leu Leu Fhr Ash Asp App GLy The (iii) Net Arg GTy Ser GTy Va. Arg The Leu Leu Fhr Ash Asp App GLy The (iii) Phe Ala Gla GT CGG GGG GGT CTG CGC AAC GTG GAG CGC GTG GGT (iii) Phe Ala Gla GTy Leu GTy Ala Leu Arg Lys Met Leu Glu Pro Val Ala (iii) Phe Ala Gla GTy Leu GTy Ala Leu Arg Lys Met Leu Glu Pro Val Ala (iii) Phe Ala Gla GTY Leu GTy Ala Leu Arg Lys Met Leu GGG GGC AGC GAT (iii) Phe Ala Gla GTY Val Val Ali Pro Asp Ala GTG CGG GAG GGC GAC GAT (iii) Phe Ala Gla GTY Val Val Ali Pro Asp Ala GTG CGG GAG GGC GAC GAT (iii) Phe Ala GTG CGC GGC GGC GGC GGG GAG GGC GAC GAT (iii) Phe Ala GTG CAC GGT CAC CGC CGC CGG GGG GAG GGG GAG GGC GAC GA		,	iiv	MODEL MODEL		TYP	F: 0	lenon	ilo 1	NA								
(1) (2) NAME/KEY; Coding Sequence																		
(8) DECEMBER DESCRIPTION: SEG TO NOT 19: (1) ATO AGG GOD AGG GAA GTG GOG ATA STT CYC ACC AAC GYT GAG GGC FIC (1) ATO AGG GOD AGG GAA GTG GOG ATA STT CYC ACC AAC GYT GAG GGC FIC (1) Bet Ang Gly Ser Gly Va. Ang The Leu Gog Fin Ash Asp App Gly The (1) 10 10 10 10 10 10 10 10 10 10 10 10 10		,	/	7.1	NA1	1E / K.E	ev: 0	odir	iq Se	-वस-ा	iCe.							
(xi) SECURNCE DESCRIPTION: SEC ID No. 19: 18: 17: ATG AGG GOG AGG GCA GTG COG ATA CTT CCC AGC AAC GTT GAG GGC FIC 18: 18: ATG AGG GOG AGG GCA GTG COG ATA CTT CCC AGC AAC GTT GAG GGC FIC 18: 19: 19: 10:										•								
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L:27 M:220 C: Keyword misspelled or invalid format. [(A) APPLICATION NUMBER:] L:28 M:220 C: Keyword misspelled or invalid format. [(B) FILING DATE:]